

Figure 1A.

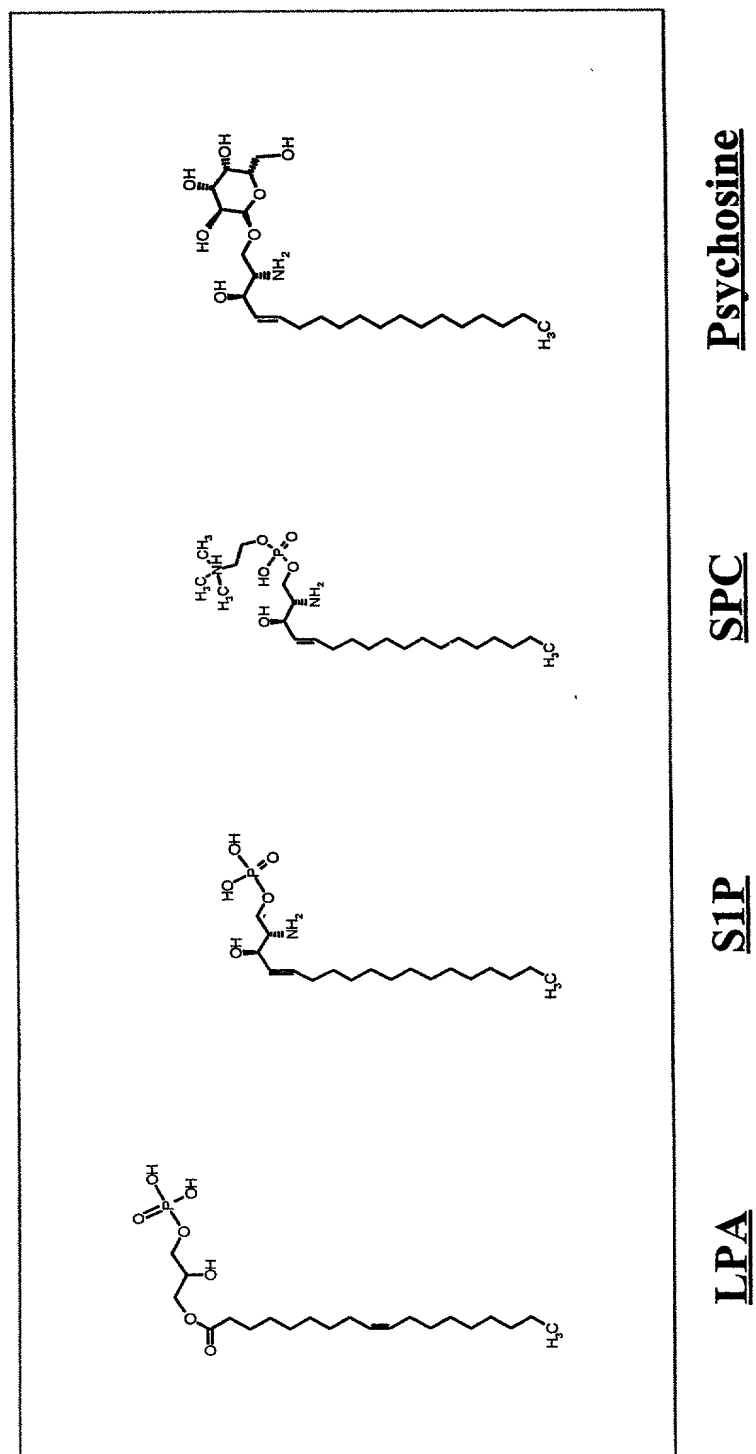


Figure 1B.

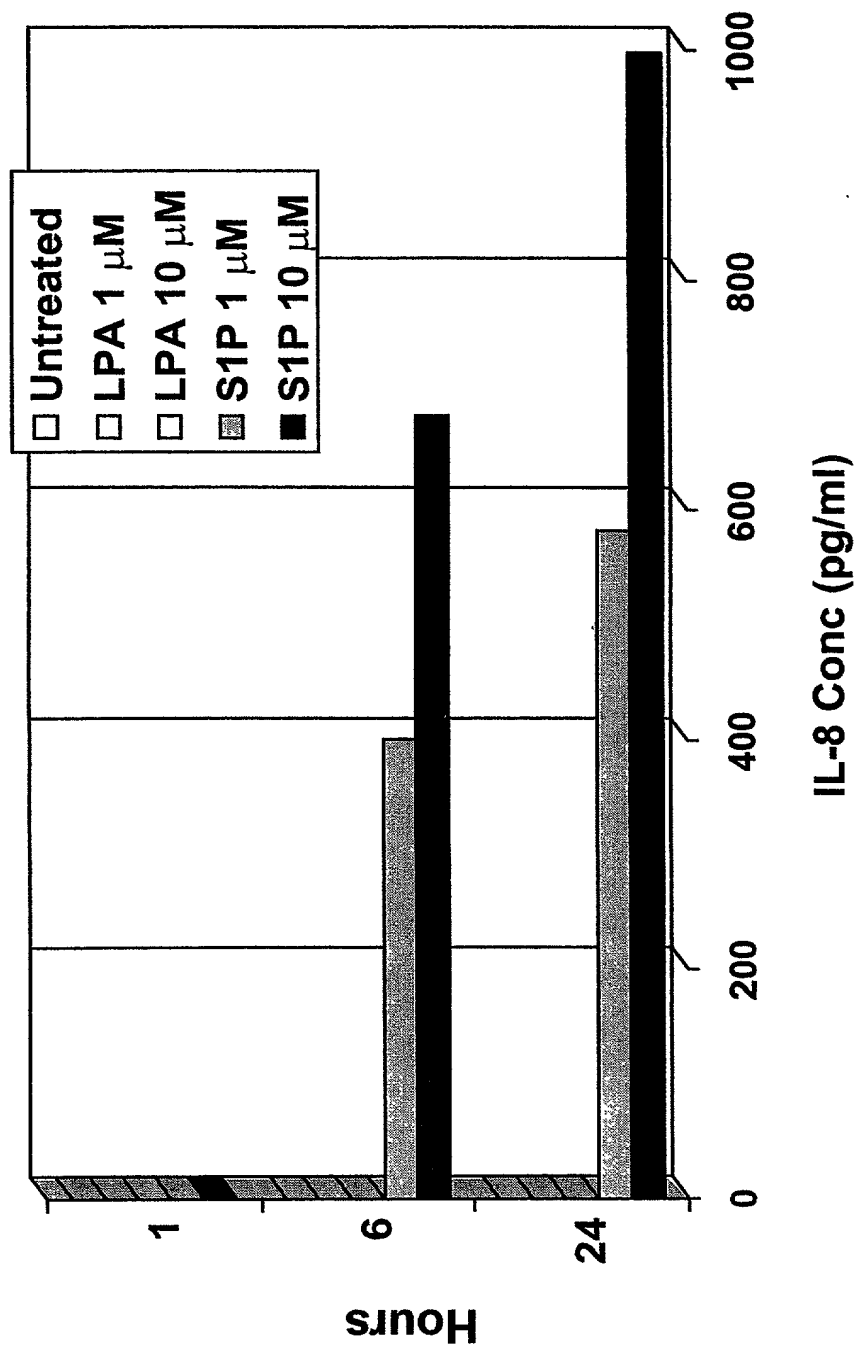
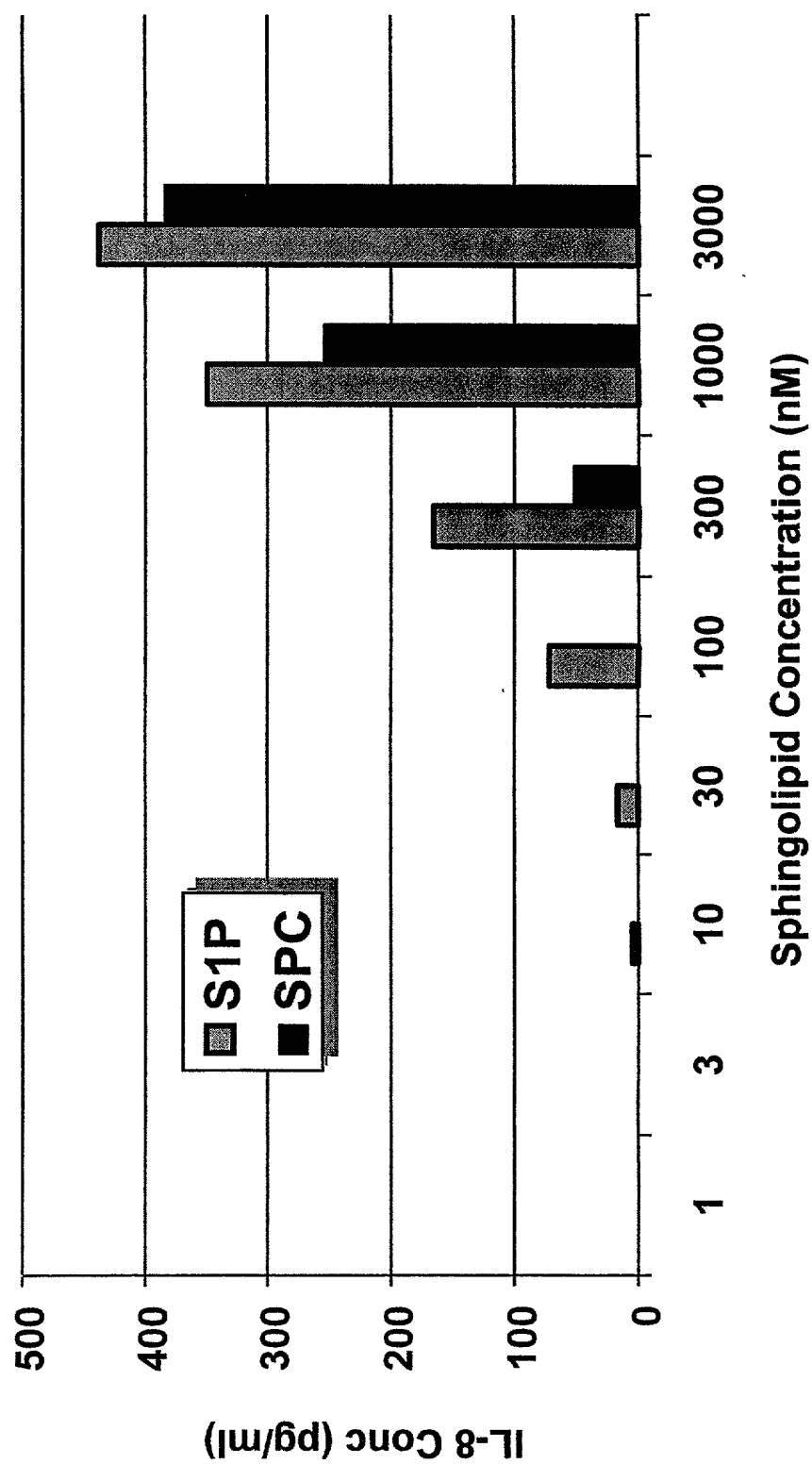


Figure 2A.



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FIGURE 2

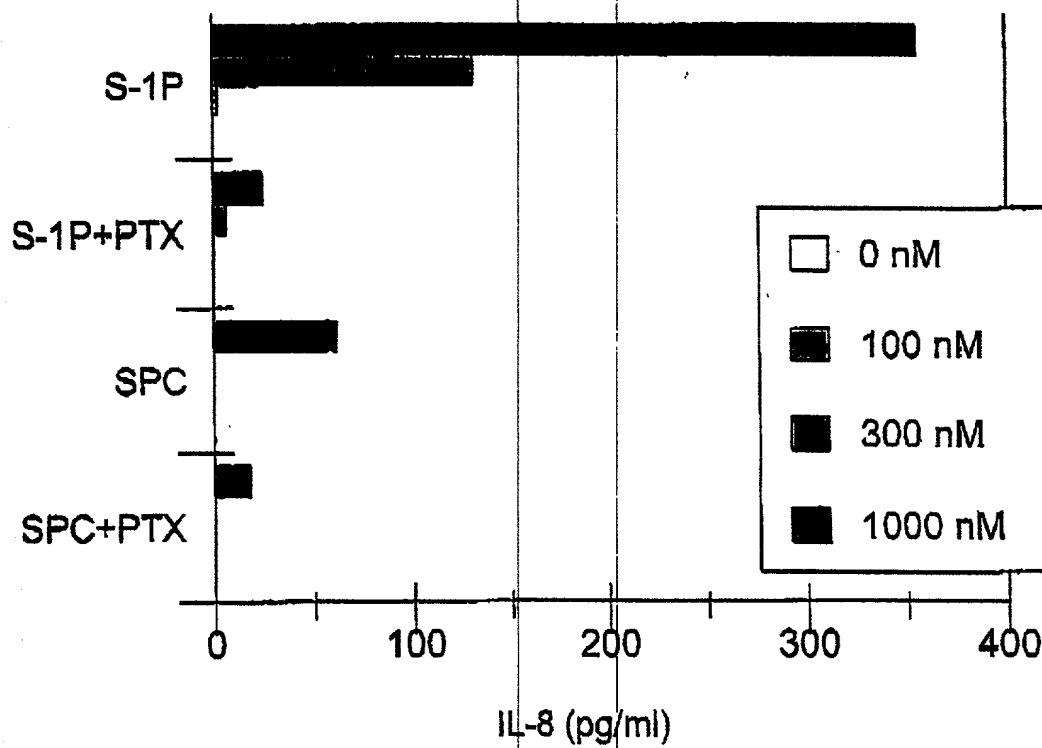


Figure 3.

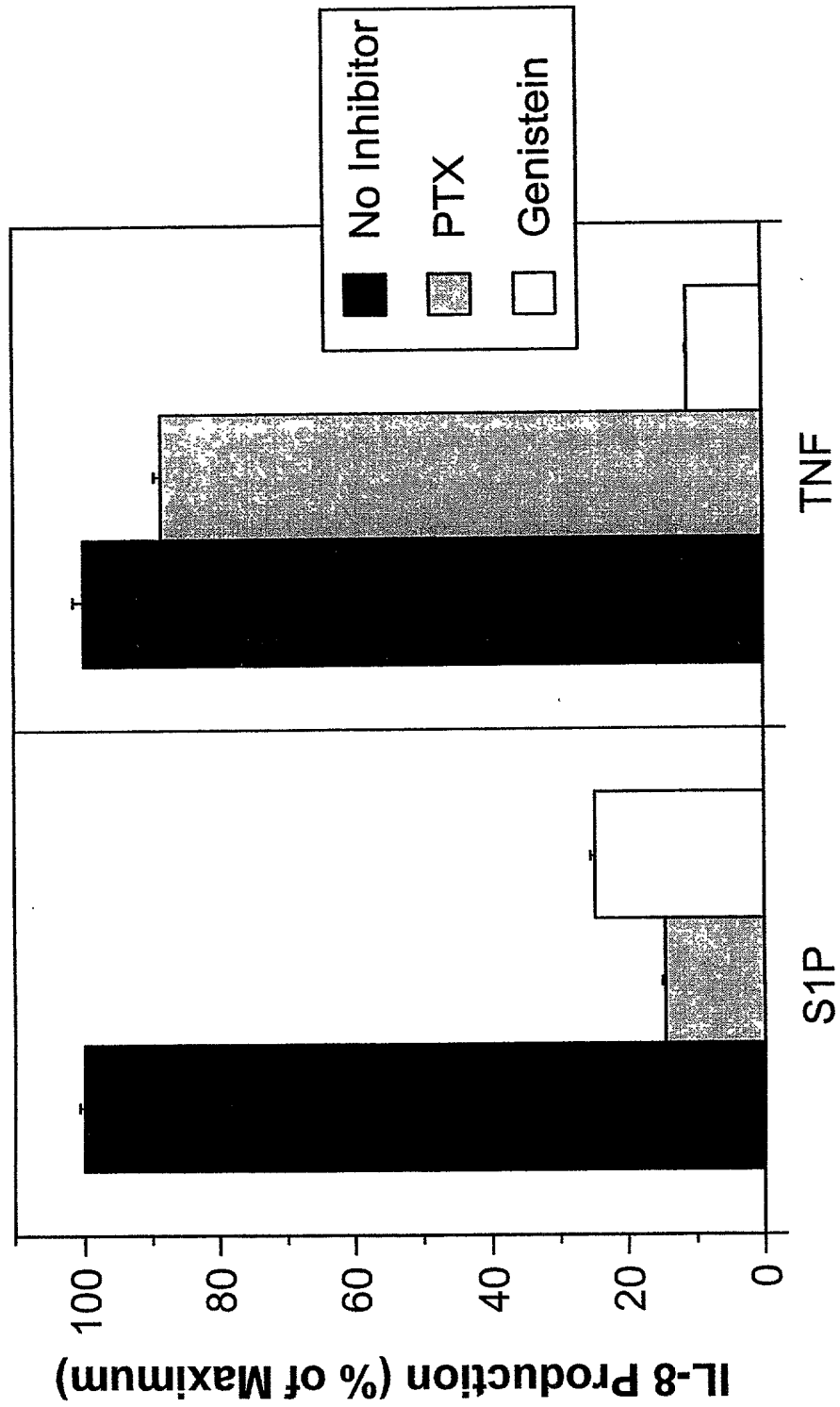


FIGURE 4A

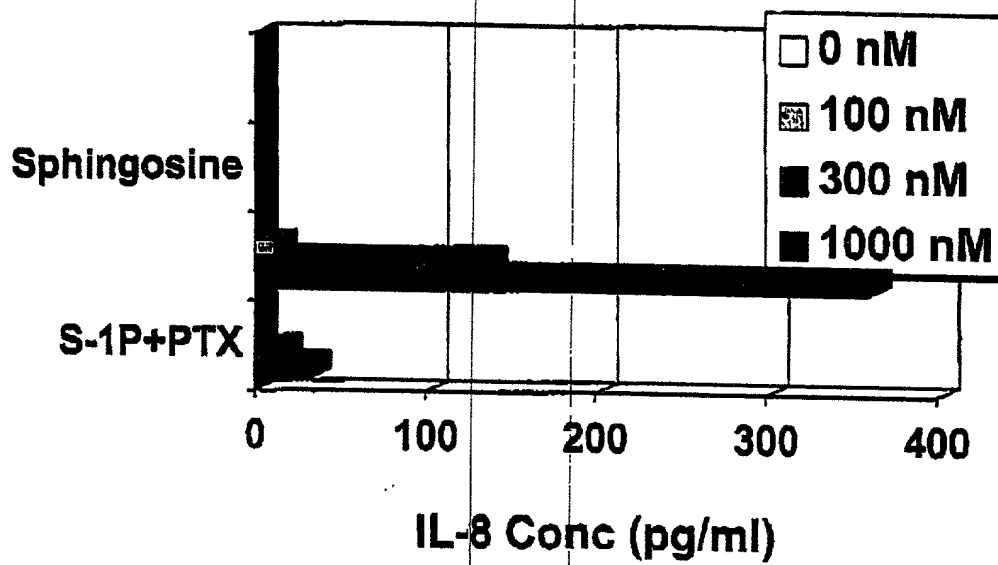


Figure 4B.

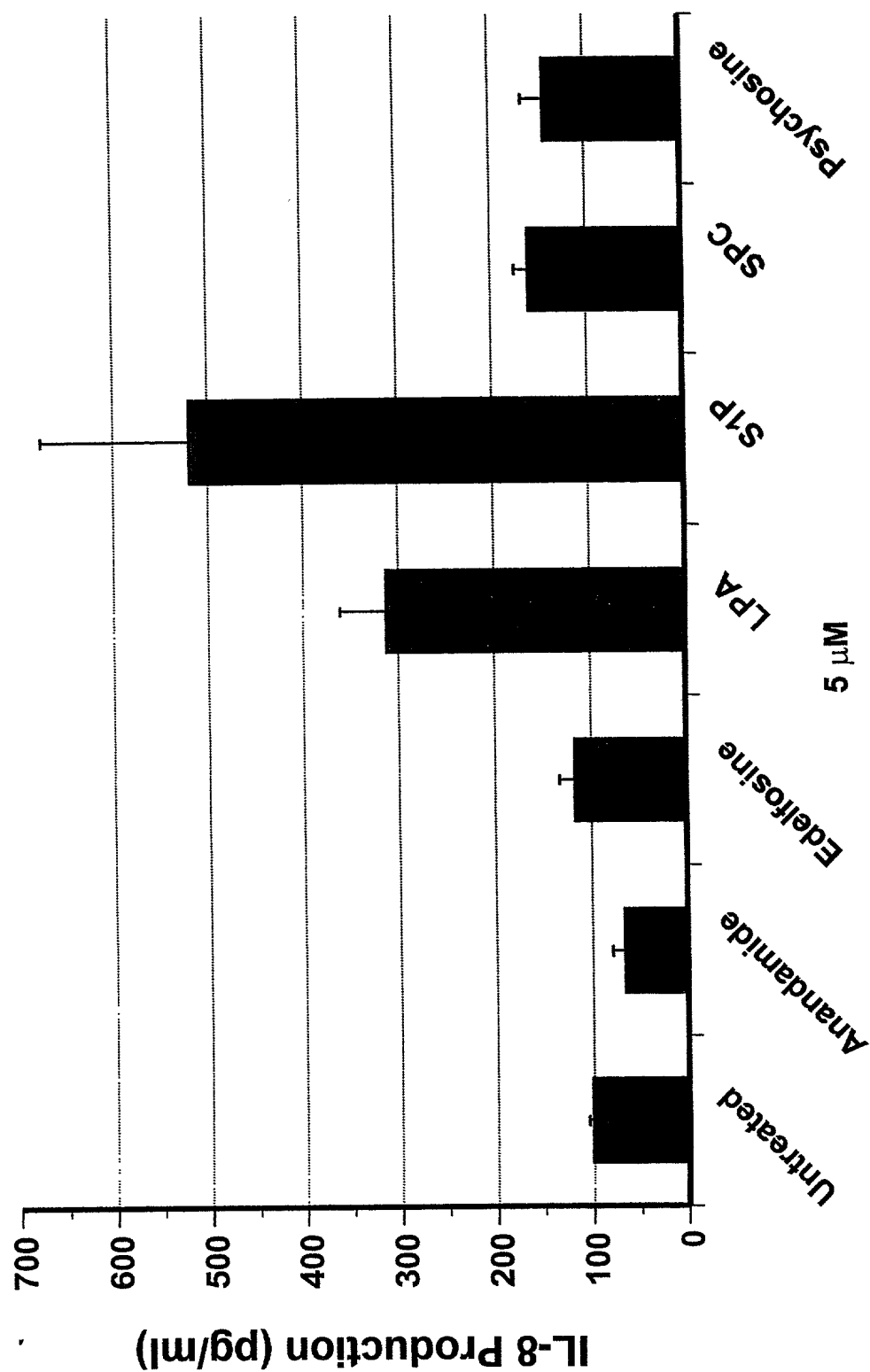


Figure 5.

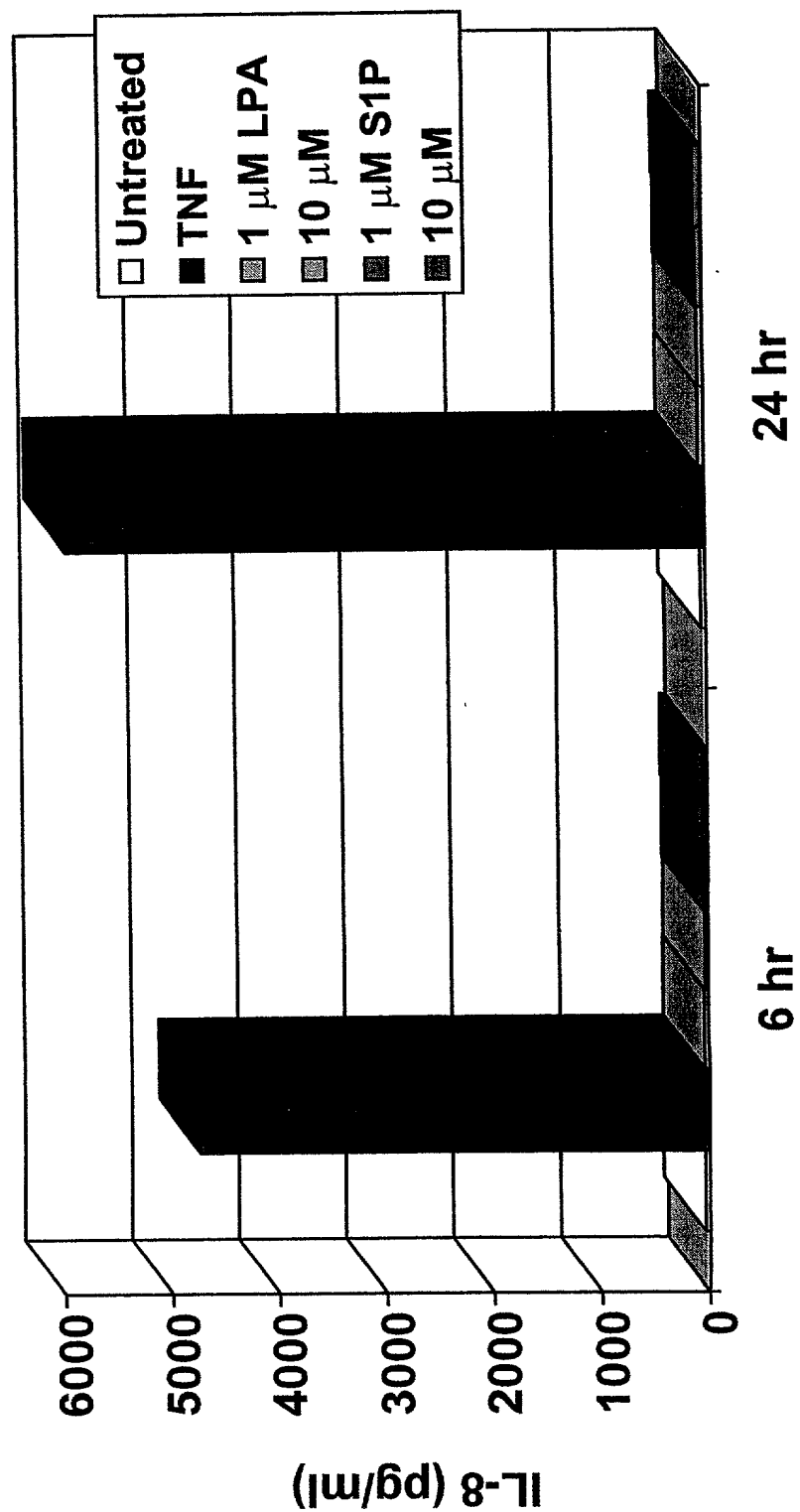


Figure 6.

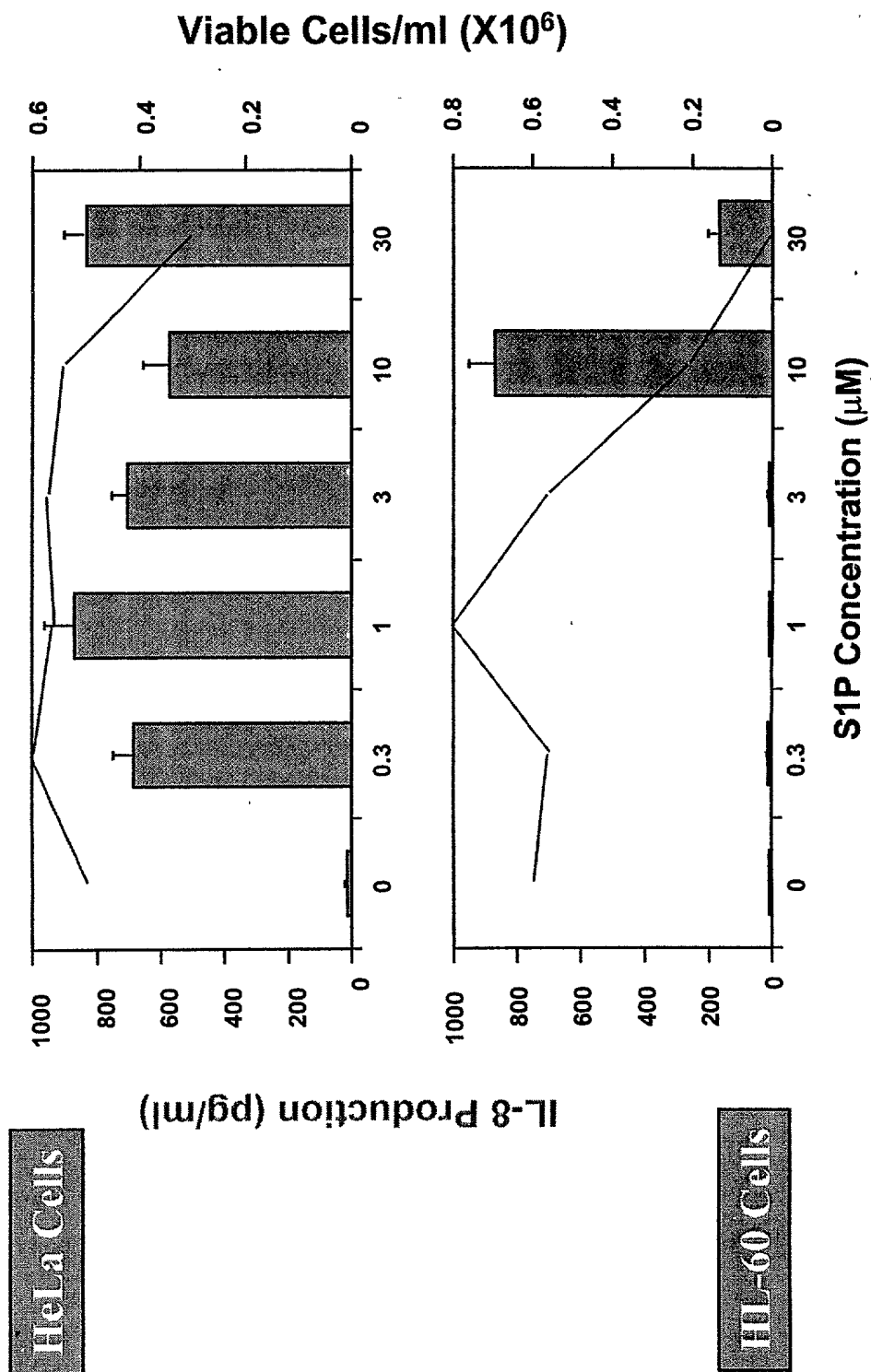


Figure 7.

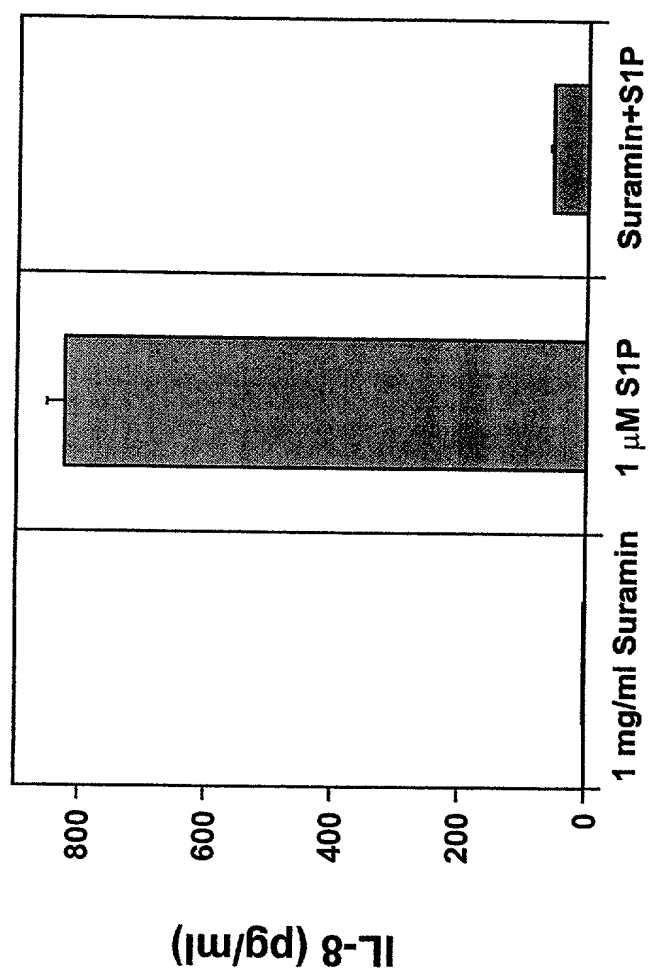


Figure 8.

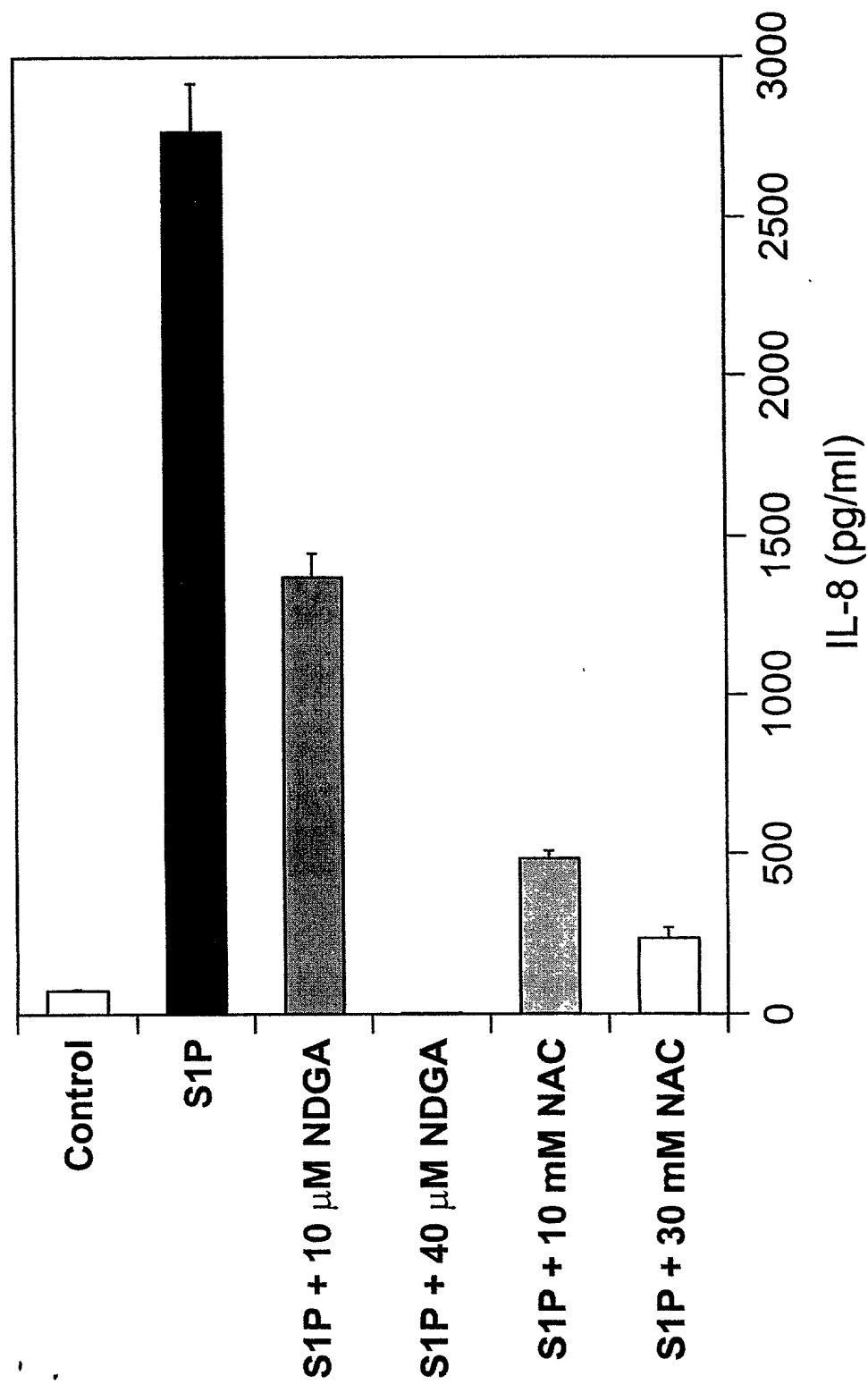


Figure 9.

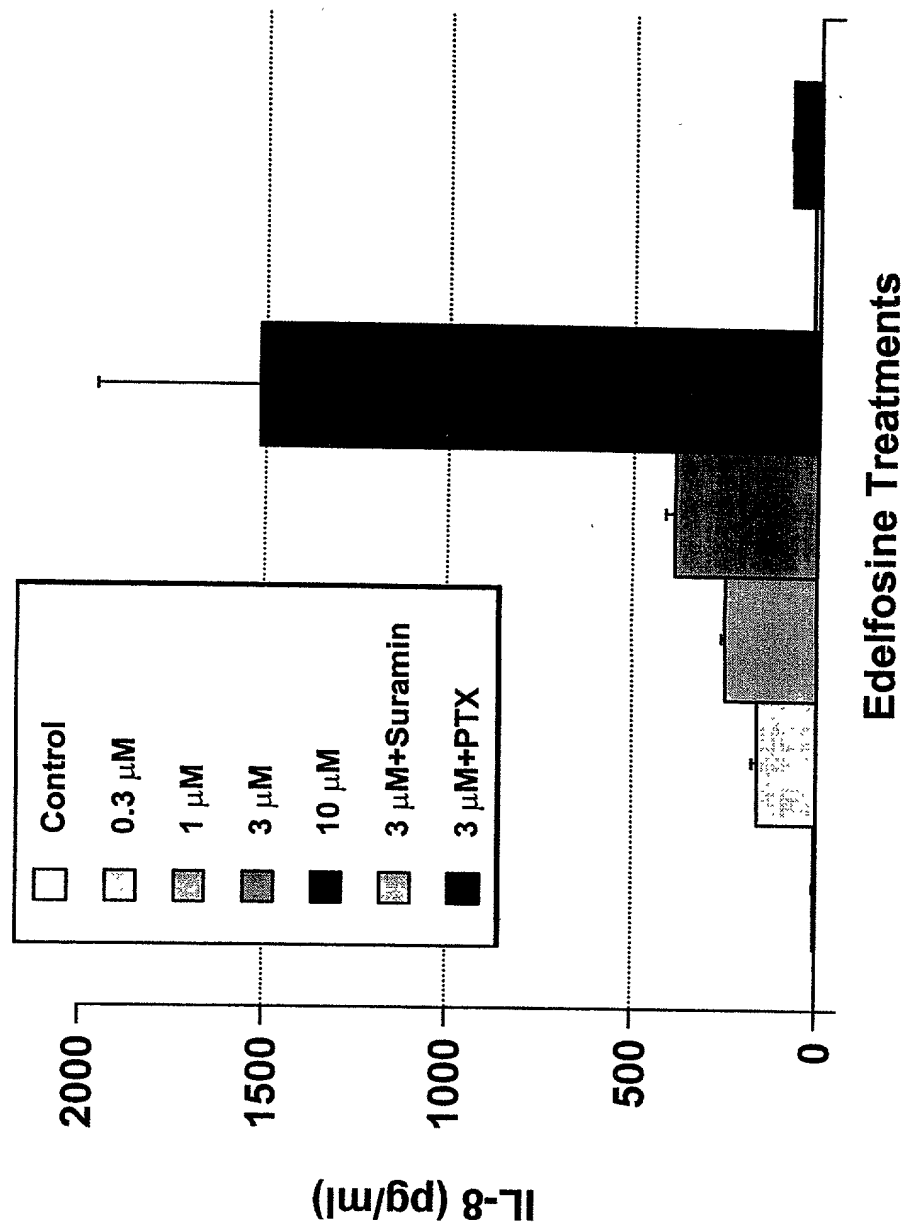


FIGURE 10A

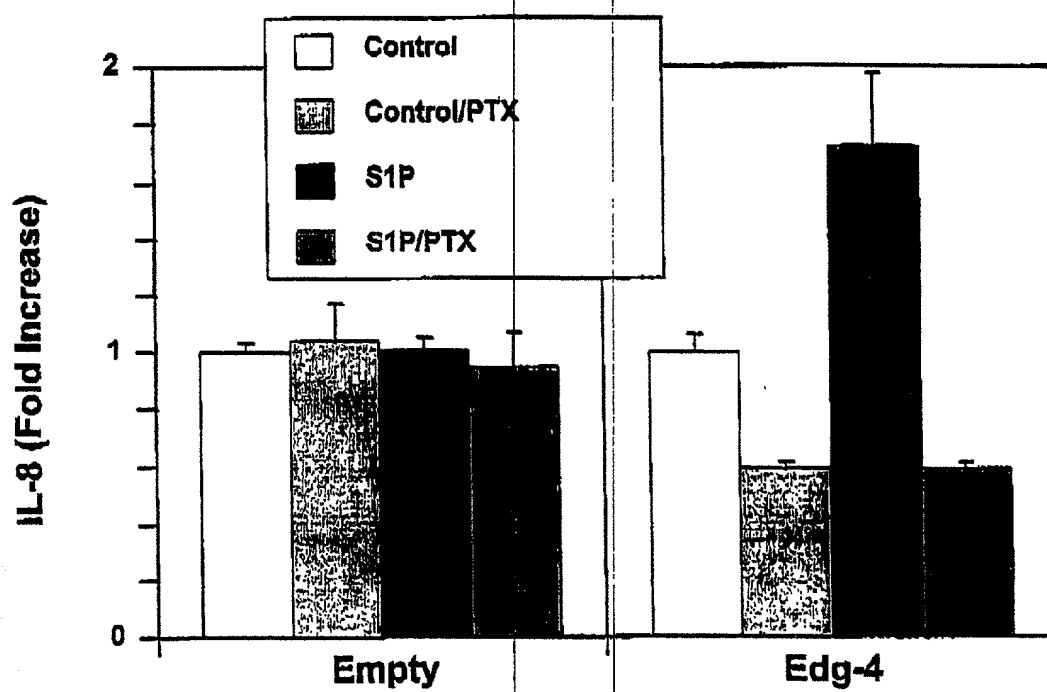


Figure 11.

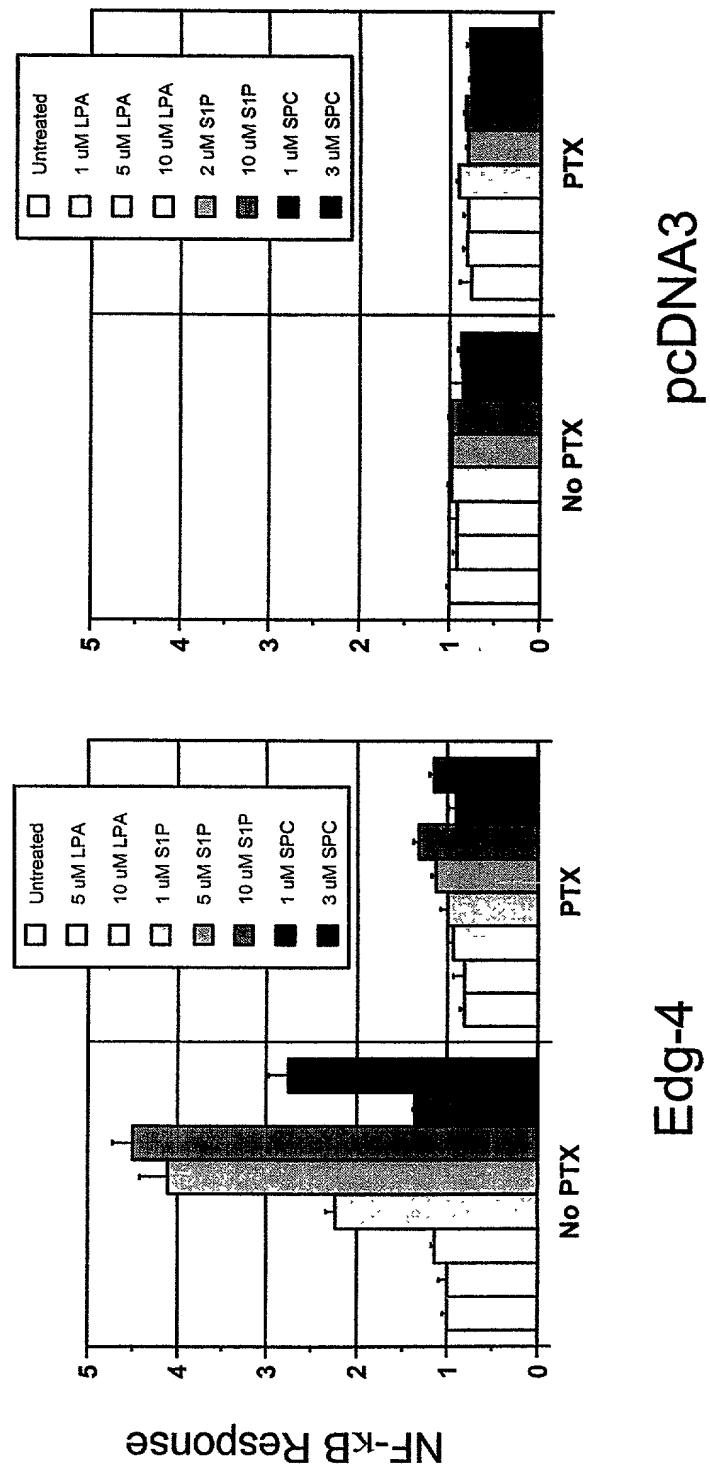


Figure 12.

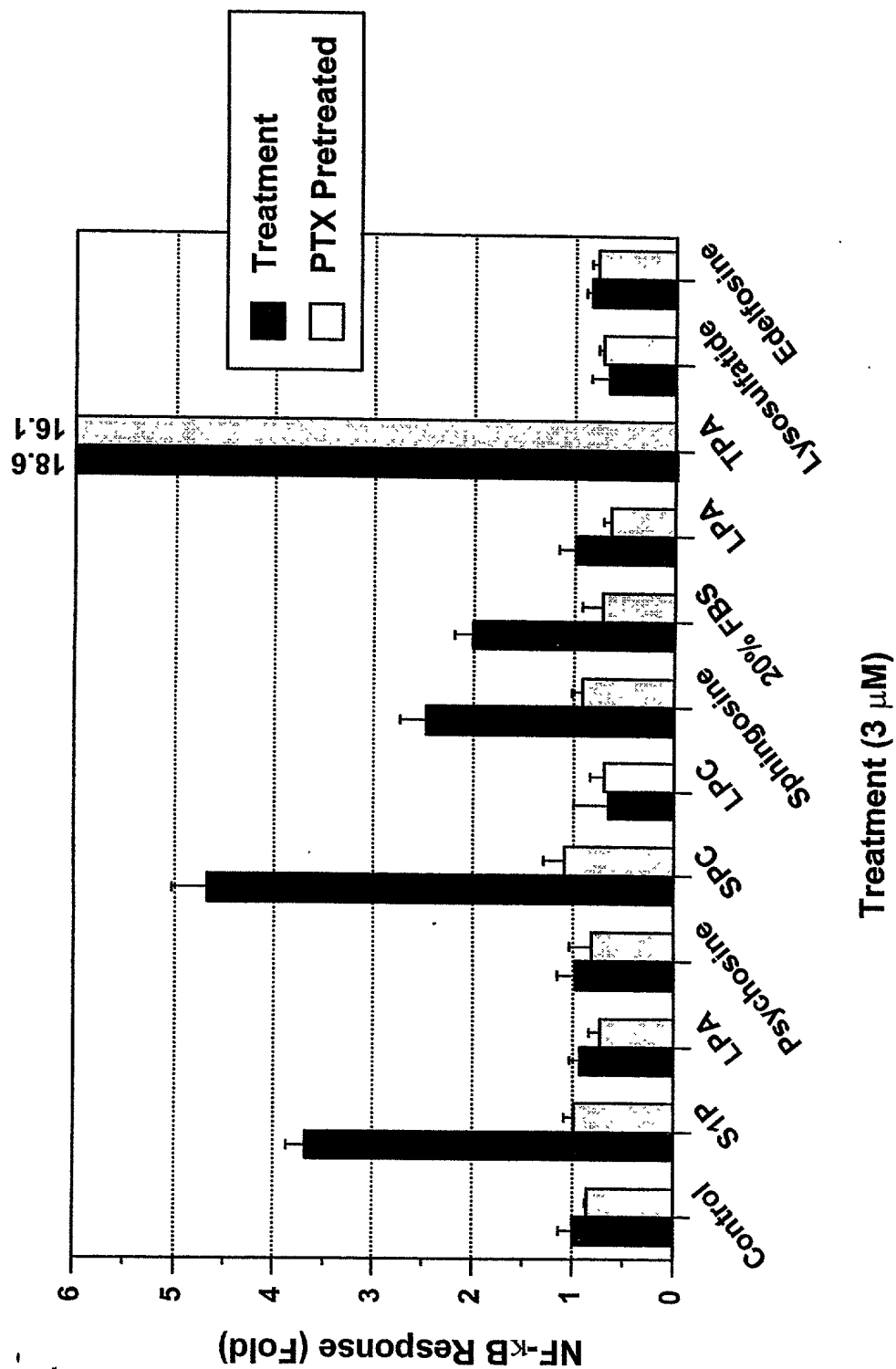
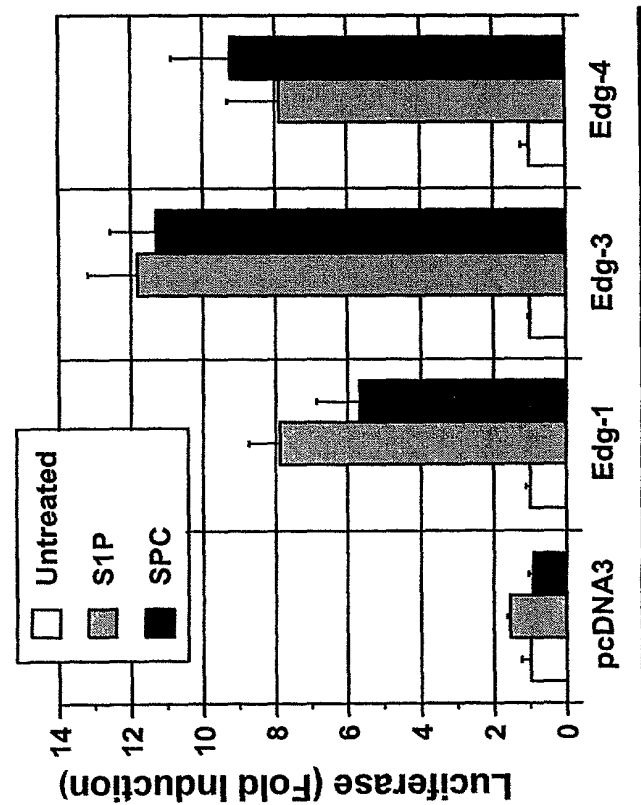
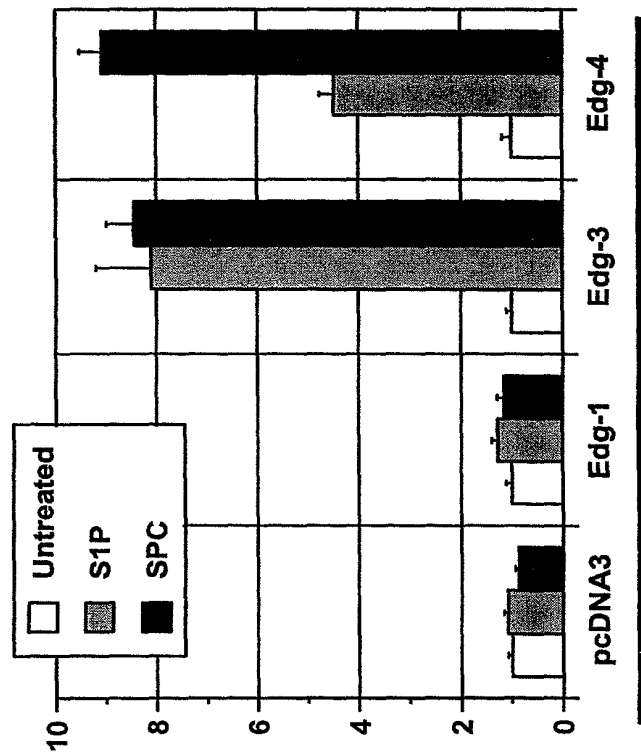


Figure 13.



SRE Reporter



NF-κB Reporter

FIGURE 14

1				50
AA834537	-----AAA	GCCCCATGGC	CCCAGCAGGC	CTCTGAGCCC CACCATGGGC
AA804628	-----AAA	GCCCCATGGC	CCCAGCAGGC	CTCTGAGCCC CACCATGGGC
AA827835	AGTTCTGAAA	GCCCCATGGC	CCCAGCAGGC	CTCTGAGCCC CACCATGGGC
	51			100
AA834537	AGCTTGTTACT	CGGAGTACCT	GAACCCCAAC	AAGGTCCAGG AACACTATAA
AA804628	AGCTTGTTACT	CGGAGTACCT	GAACCCCAAC	AAGGTCCAGG AACACTATAA
AA827835	AGCTTGTTACT	CGGAGTACCT	GAACCCCAAC	AAGGTCCAGG AACACTATAA
	101			150
AA834537	TTATACCAAG	GAGACGCTGG	AAACGCAGGA	GACGACCTCC CGCCAGGTGG
AA804628	TTATACCAAG	GAGACGCTGG	AAACGCAGGA	GACGACCTCC CGCCAGGTGG
AA827835	TTATACCAAG	GAGACGCTGG	AAACGCAGGA	GACGACCTCC CGCCAGGTGG
	151			200
AA834537	CCTCGGCATT	CATCGTCATC	CTCTGTTGCG	CCATTGTGGT GGAAAACCTT
AA804628	CCTCGGCATT	CATCGTCATC	CTCTGTTGCG	CCATTGTGGT GGAAAACCTT
AA827835	GCTCGGCCTT	CATCGTCATC	CTCTGTTGCG	CCATTGTGGT GGAAAACCTT
	201			250
AA834537	CTGGTGCTCA	TTGCGGTGGC	CCGAAACAGC	AAGTTCCACT CGGCAATGTA
AA804628	CTGGTGCTCA	TTGCGGTGGC	CCGAAACAGC	AAGTTCCACT CGGCAATGTA
AA827835	CTGGTGCTCA	TTGCGGTGGC	CCGAAACAGC	AAGTTCCACT CGGCAATGTA
	251			300
AA834537	CCTGTTTCTG	GGCAACCTGG	CCGCCCTCCG	TCTACTGGCA GGCCTGGCCT
AA804628	CCTGTTTCTG	GGCAACCTGG	CCGCCCTCCG	TCTACTGGCA GGCCTGGCCT
AA827835	CCTGTTTCTG	GGCAACCTGG	CCGCCCTCCG	TCTACTGGCA GGCCTGG. CT
	301			350
AA834537	TCGTAGCCAA	TACCTTGCTC	TCTGGCTCTG	TCACGCTGAG GCTGACGCCT
AA804628	TCGTAGCCAA	TACCTTGCTC	TCTGGCTCTG	TCACGCTGAG GCTGACGCCT
AA827835	TCGTAGCCAA	TACCTTGCTC	TCTGGCTCTG	TCACGCTGAG GCTGACGCCT
	351			400
AA834537	GTGCAGTGGT	TTGCCCGGGA	CGGTCTGCCT	TCATCAGCCT CTCGGCCTCT
AA804628	GTGCAGTGGT	TTGCCCGGGA	C-----	-----
AA827835	GTGCAGTGGT	TTGCCCGGGA	-----	-----
	401			450
AA834537	GTCTTCAGCC	TCCTGGCCAT	CGCCATTGAG	CGCCACGTGG CCATTGCAAA
AA804628	-----	-----	-----	-----
AA827835	-----	-----	-----	-----
	451			
AA834537	GG			
AA804628	--			
AA827835	--			

10084507.022602

FIGURE 15 A

M G S L Y S E Y

1 AAAGCCCCATGGCCCCAGCAGGCCTCTGAGCCCCACCATGGGCAGCTTGTACTCGGAGTA 60
 -----+-----+-----+-----+-----+
 TTTCCGGGGTACCGGGGTCGTCCGGAGACTCGGGGTGGTACCCGTCCGAACATGAGCCTCAT

61 L N P N K V Q E E Y N Y T K E T L E T Q 120
 CCTGAACCCCAACAGGTCCAGGAACACTATAATTATACCAAGGAGACGCTGGAAACGCA
 -----+-----+-----+-----+-----+
 GGAATTGGGGTTGTTCCAGGTCCTTGTGATATTAATATGGTTCTCTCGGACCTTTGCGT

121 E T T S R Q V A S A F I V I L C C A I V 180
 GGAGACGACCTCCCGCCAGGTGGCCTCGGGCTTCATCGTTCATCCTCTGTTGCGCCATTGT
 -----+-----+-----+-----+-----+
 CCTCTGCTGGAGGGCGGTCCACCGGAGCCGGAAGTAGCAGTAGGAGACAACGCGGTAACA

161 V E N L L V L I A V A R N S K F E S A M 240
 GGTGGAAAACCTTCTGGTGCTCATTCGCGTGGCCCGAAACAGCAAGTTCCACTCGGCAAT
 -----+-----+-----+-----+-----+
 CCACCTTTTGGAGACCACGAGTAACGCCACCGGGCTTGTGCTTCAAGGTGAGCCGTTA

241 Y L F L G N L A A S D L L A G V A F V A 300
 GTACCTGTCTTCTGGGCAACCTGGCCCGCTCCGATCTACTGGCAGGCGTGGCCTTCTGTAGC
 -----+-----+-----+-----+-----+
 CATGGACAAAGACCCGTTGGACCGGCGGAGGCTAGATGACCGTCCGACCGGAAGCATCG

301 N T L L S G S V T L R L T P V Q W F A R 360
 CAATACCTTGCTCTCTGGCTCTGTCCAGCTGAGGCTGACCCCTGTGCACTGGTTTGGCCG
 -----+-----+-----+-----+-----+
 GTTATGGAACGAGAGACCGAGACAGTGCGACTCCGACTGCGGACACGTCAACAAACGGGC

361 E G S A F I T L S A S V F S L L A I A I 420
 GGAGGGCTCTGCTTCATCACGCTCTCGGCCTCTGTCTTCAGCCTCTGGCCATCGCCAT
 -----+-----+-----+-----+-----+
 CCTCCCGAGACGGAAGTAGTGCGAGAGCCGGAGACAGAAGTCGGAGGACCGGTAGCGGTA

421 E R H V A I A K V K L Y G S D K S C R M 480
 TGAGCGCCACGTGGCCATTGCCAAGGTCAAGCTGTATGGCAGCGACAAGAGCTGCCGCAT
 -----+-----+-----+-----+-----+
 ACTCGCGGTGCACCGGTAACGTTCCAGTTCGACATACCGTCTGTCTCTCGACGGCGTA

481 L L L I G A S W L I S L V L G G L P I L 540
 GCTTCTGCTCATCGGGGCTCGTGGCTCATCTCGCTGCTCGCTGGGCTGGCCATCCT
 -----+-----+-----+-----+-----+
 CGAAGACGAGTAGCCCCGGAGCACCGAGTAGAGCGACAGGAGCCACCGACGGGTAGGA

541 G W N C L G H L E A C S T V L P L Y A K 600
 TGGCTGGAACTGCCTGGGCCACCTCGAGGCTGCTCCACTGTCTCTGCTCTCTACGCCAA
 -----+-----+-----+-----+-----+
 ACCGACCTTGACGGACCCGCTGGAGCTCCGACGAGGTGACAGGACGGAGAGATGCGGTT

601 H Y V L C V V T I F S I I L L A I V A L 660
 GCATTATGTGCTGTCGCTGGTGACCATCTCTCCATCATCCTGTTGGCCATCGTGGCCCT
 -----+-----+-----+-----+-----+
 CGTAATACACGACACGCCACCACTGGTAGAGAGGTAGTAGGACAACCGGTAGCACCGGGA

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	Y V R I Y C V R S S H A D M A A P Q T	
561	GTACGTCGCATCTACTGCGTGGTCCGCTCAAGCCACGCTGACATGGCCGCCCGCAGAC -----+-----+-----+-----+	720
	CATGCACGCGTAGATGACGCACCAGGCGAGTTCEGTCGCACTGTACCGGGCGGGCGTCTG	
	L A L L K T V T I V L G V F I V C W L P	
721	GCTAGCCCTGCTCAAGACGCTCACCATCGTGCTAGGCGTCTTTTATCGTCTGCTGGCTGCC -----+-----+-----+-----+	780
	CGATCGGGGACGAGTTCTGCCAGTGGTAGCAGGATCCGCAGAAATAGCAGACGACCGACGG	
	A F S I L L L D Y A C P V H S C P I L Y	
781	CGCCTTCAGCATCGTCCTTCTGGACTATGCTGTCCCCTCCACTCCTGCCCGATCCTCTA -----+-----+-----+-----+	840
	GCGGAAGTCGTAGGAGGAAGACCTGATACGGACAGGGCAGGTGAGCAGCGGCTAGGAGAT	
	K A H Y (X) F A V S T L N S L L N P V I Y	
841	CAAAGCCCCACTACTTTTTTCGCCGCTCTCCACCGCTGAATTCCCTGCTCAACCCCGTCACTTA -----+-----+-----+-----+	900
	GTTTCGGGTGATGRAAAAGCGGCAGAGGTGGGACTTAAGGGACGAGTTGGGGCAGTAGAT	
	T W R S R D L R R E V L R P L Q C W R P	
901	CACGTGGCGCAGCCGGGACCTGCGCGCGGAGGTGCTTCGGCCGCTGCAGTGCTGGCGGCC -----+-----+-----+-----+	960
	GTGCACCGCGTCGGCCCTGGACGCGCGCCCTCCACGAAGCCGGCGACGTNACGACCGCCGG	
	G V G V Q G R R R G G T F G H H L L P L	
961	GGGGGTGGGGGTGCAGGACGGAGGCGGGGGCGGGACCCGGGGCCACCACCTCCTGCCACT -----+-----+-----+-----+	1020
	CCCCACCCCCACGTTCTCTGCCTCCGCCCCGCCCTGGGGCCCGGTGGTGGAGGACGGTGA	
	R S S S S L E R G M H M P T S P T F L E	
1021	CCGCAGCTCCAGCTCCCTGGAGAGGGGCATGCACATGCCACGTCACCCACGTTTCTGGA -----+-----+-----+-----+	1080
	GCGCTCGAGGTCGAGGGACCTCTCCCCGTACGTGTACGGGTGCAGTGGGTGAAAAGACCT	
	G N T V V *	
1081	GGGCAACACGGTGGTCTGAGGGTGGGGGTGGACCAACAACAGGCCAGGGCATAGGGGTT -----+-----+-----+-----+	1140
	CCCGTTGTGCCACGAGACTCCACCCCCACCTGGTTGTTGGTCCGGTCCCGTATCCCCAA	
1141	CATGGAAAGGCCACTGGGTGACCCCAAATA -----+-----+-----+-----+	1170
	GTACCTTTCCGGTGACCCACTGGGGTTTAT	

Figure 15B

cDNA sequence of clone pC3-hedg4#36 encoding functional HEDG4 receptor protein.

10084507.022800

```
1  ATGGGCAGCTTGTACTCGGAGTACCTGAACCCCAACAAGGTCCAGGAACACTATAATTAT 60
   -----+-----+-----+-----+-----+-----+
61  TACCCGTCGAACATGAGCCTCATGGACTTGGGGTTGTTCCAGGTCCTTGTGATATTAATA
   -----+-----+-----+-----+-----+-----+
   ACCAAGGAGACGCTGGAAACGCAGGAGACGACCTCCCGCCAGGTGGCCTCGGCCTTCATC 120
   -----+-----+-----+-----+-----+-----+
   TGGTTCCTCTGCGACCTTTGCGTCTCTGCTGGAGGGCGGTCCACCGGAGCCGGAAGTAG
   -----+-----+-----+-----+-----+-----+
121  GTCATCCTCTGTTGCGCCATTGTGGTGGAAAACCTTCTGGTGCTCATTGCGGTGGCCCCGA
   -----+-----+-----+-----+-----+-----+
   CAGTAGGAGACAACCGGTAACACCACCTTTTGAAGACCACGAGTAACGCCACCGGGCT
   -----+-----+-----+-----+-----+-----+
181  AACAGCAAGTTCCACTCGGCAATGTACCTGTTTCTGGGCAACCTGGCCGCCTCCGATCTA
   -----+-----+-----+-----+-----+-----+
   TTGTCGTTCAAGGTGAGCCGTTACATGGACAAAGACCCGTTGGACCGGCGGAGGCTAGAT
   -----+-----+-----+-----+-----+-----+
241  CTGGCAGGCGTGGCCTTCGTAGCCAATACCTTGCTCTCTGGCTCTGTCACGCTGAGGCTG
   -----+-----+-----+-----+-----+-----+
   GACCGTCCGCACCGGAAGCATCGGTTATGGAACGAGAGACCGAGACAGTGCGACTCCGAC
   -----+-----+-----+-----+-----+-----+
301  ACGCCTGTGCAGTGGTTTGGCCGGGAGGGCTCTGCCTTCATCACGCTCTCGGCCTCTGTC
   -----+-----+-----+-----+-----+-----+
   TGCGGACACGTCACCAAACGGGCCCTCCCGAGACGGAAGTAGTGCAGAGCCGGAGACAG
   -----+-----+-----+-----+-----+-----+
361  TTCAGCCTCCTGGCCATCGCCATTGAGCGCCACGTGGCCATTGCCAAGGTCAAGCTGTAT
   -----+-----+-----+-----+-----+-----+
   AAGTCGGAGGACCGGTAGCGTAACCTCGCGGTGCACCGGTAACGGTTCCAGTTCGACATA
   -----+-----+-----+-----+-----+-----+
421  GGCAGCGACAAGAGCTGCCGCATGCTTCTGCTCATCGGGGCCTCGTGGCTCATCTCGCTG
   -----+-----+-----+-----+-----+-----+
   CCGTCGCTGTTCTCGACGGCGTACGAAGACGAGTAGCCCCGGAGCACCGAGTAGAGCGAC
   -----+-----+-----+-----+-----+-----+
481  GTCTCTCGGTGGCCTGCCCATCCTTGGCTGGAACTGCCTGGGGCCACCTCGAGGCCTGCTCC
   -----+-----+-----+-----+-----+-----+
   CAGGAGCCACCGGACGGGTAGGAACCGACCTTGACGGACCCGGTGGAGCTCCGGACGAGG
   -----+-----+-----+-----+-----+-----+
541  ACTGTCCTGCCTCTCTACGCCAAGCATTATGTGCTGTGCGTGGTGACCATCTTCTCCATC
   -----+-----+-----+-----+-----+-----+
   TGACAGGACGGAGAGATGCGGTTGTAATACACGACACGCACCACTGGTAGAAGAGGTAG
   -----+-----+-----+-----+-----+-----+
601  ATCCTGTTGGCCGTCGTGGCCCTGTACGTGCGCATCTACTGCGTGGTCCGCTCAAGCCAC
   -----+-----+-----+-----+-----+-----+
   TAGGACAACCGGCAGCACCGGGACATGCACGCTAGATGACGCACCAGGCGAGTTCGGTG
   -----+-----+-----+-----+-----+-----+
661  GCTGACATGGCCGCCCCGAGACGCTAGCCCTGCTCAAGACGGTCACCATCGTGCTAGGC
   -----+-----+-----+-----+-----+-----+
   CGACTGTACC GGCGGGGCGTCTGCGATCGGGACGAGTTCTGCCAGTGGTAGCACGATCCG
   -----+-----+-----+-----+-----+-----+
721  GTCTTTATCGTCTGCTGGCTGCCCCGCTTCAGCATCCTCCTTCTGGACTATGCCTGTCCC
   -----+-----+-----+-----+-----+-----+
780
```

CAGAAATAGCAGACGACCGACGGGCGGAAGTCGTAGGAGGAAGACCTGATACGGACAGGG

781 GTCCACTCCTGCCCCGATCCTCTACAAAGCCCACCTACCTTTTCGCCGTCTCCACCCTGAAT
-----+-----+-----+-----+-----+-----+-----+-----+ 840
CAGGTGAGGACGGGCTAGGAGATGTTTCGGGTGATGGAAAAGCGGCAGAGGTGGGACTTA

841 TCCCTGCTCAACCCCGTCATCTACACGTGGCGCAGCCGGGACCTGCGGCGGGAGGTGCTT
-----+-----+-----+-----+-----+-----+-----+-----+ 900
AGGGACGAGTTGGGGCAGTAGATGTGCACCGCGTCGGCCCTGGACGCCGCCCTCCACGAA

901 CGGCCGCTGCAGTGCTGGCGGCCGGGGTGGGGGTGCAAGGACGGAGGCGGGGCGGGACC
-----+-----+-----+-----+-----+-----+-----+-----+ 960
GCCGGCGACGTCACGACCGCGGCCCGCCCCACCCCCACGTTCTGCTCCGCCCCGCCCTGG

961 CCGGGCCACCACCTCCTGCCACTCCGCAGCTCCAGCTCCCTGGAGAGGGGCATGCACATG
-----+-----+-----+-----+-----+-----+-----+-----+ 1020
GGCCCGGTGGTGGAGGACGGTGAGGCGTCGAGGTCGAGGGACCTCTCCCCGTACGTGTAC

1021 CCCACGTCACCCACGTTTCTGGAGGGCAACACGGTGGTCTGA
-----+-----+-----+-----+-----+-----+-----+-----+ 1062
GGGTGCAGTGGGTGCAAAGACCTCCCGTTGTGCCACCAGACT

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FIGURE 16 A

1 MGSLYSEYLN PNKVOEHYNY TKETLETOET TSQVASAFI VILCCAIVVE
 51 NLLVLIIVAR NSKPHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL
 101 TFWQWFAREG SAFITLSAEV FSLIAIAIER HVAIAKVLY GSDKSCRMLL
 151 LIGASWLISL VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLGCVVTIESI
 201 ILLAIVALYV RIYCVVRSRH ADMAAPQTLA LLKTVTVILG VFIVCWLPAP
 251 SILLDDYACP VHSCPILYKA HYKFAVSTLN SLLAPVIYTW RSRDLRREVL
 301 RFLQCWRPGV GVQGERRGGT PGHLLPLRS SSSLERGMMH PTSFTFLEGN
 351 TVV*

Conserved features of G-protein coupled receptors include:

N-terminal extracellular domain:	Residues 1 - 36
TM-I:	Residues 37 - 57
Intracellular loop 1:	Residues 58 - 68
TM-II:	Residues 69 - 92
Extracellular loop 1:	Residues 93 - 111
TM-III:	Residues 112 - 130
Intracellular loop 2:	Residues 131 - 149
TM-IV:	Residues 150 - 168
Extracellular loop 2:	Residues 169 - 185
TM-V:	Residues 186 - 210
Intracellular loop 3:	Residues 211 - 232
TM-VI:	Residues 233 - 254
Extracellular loop 3:	Residues 255 - 266
TM-VII:	Residues 267 - 285
C-terminal cytoplasmic domain:	Residues 286 - 353

Potential post-transcriptional modification sites:

N-glycosylation:	Residues 19
Phosphorylation:	Residues 142, 145, 219, 289, 332, 345
Myristylation:	Residues 141, 318

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Figure 16B

Predicted amino acid sequence of HEDG4 polypeptide encoded by pC3-hedg4#36.

1 MGSLYSEYLN PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE
51 NLLVLIAVAR NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL
101 TPVQWFAREG SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL
151 LIGASWLISL VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI
201 ILLAVVALYV RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAF
251 SILLLDYACP VHSCPILYKA HYLFAVSTLN SLLNPVIYTW RSRDLRREVL
301 RPLQCWRPGV GVQGRRRGGT PGHHLLPLRS SSSLERGMHM PTSPTFLEGN
351 TVV

10084507.DP2E02

Figure 17B

Alignment of HEDG4 with pC3-hedg4#36 translation product and rat H218 (REDG4). Differences between pC3-hedg4#36 translation product and previously determined HEDG4 polypeptide are indicated in reverse text. Differences between rat and human edg-4 polypeptide sequences are shown in bold, shaded text.

	1		50
HEDG4	MGS	LYSEYLN	PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE
HEDG4#36	MGS	LYSEYLN	PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE
REDG4	MGS	LYSEYLN	PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE
	51		100
HEDG4	NLLVLI	AVAR	NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL
HEDG4#36	NLLVLI	AVAR	NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL
REDG4	NLLVLI	AVAR	NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL
	101		150
HEDG4	TPVQWF	AREG	SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL
HEDG4#36	TPVQWF	AREG	SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL
REDG4	TPVQWF	AREG	SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL
	151		200
HEDG4	LIGASWL	ISL	VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI
HEDG4#36	LIGASWL	ISL	VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI
REDG4	LIGASWL	ISL	VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI
	201		250
HEDG4	ILLAVVAL	YV	RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAP
HEDG4#36	ILLAVVAL	YV	RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAP
REDG4	ILLAVVAL	YV	RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAP
	251		300
HEDG4	SILLLDY	ACP	VHSCPILYKA HYXFAVSTLN SLLNPVIYTW RSRDLRREVL
HEDG4#36	SILLLDY	ACP	VHSCPILYKA HYXFAVSTLN SLLNPVIYTW RSRDLRREVL
REDG4	SILLLDY	ACP	VHSCPILYKA HYXFAVSTLN SLLNPVIYTW RSRDLRREVL
	301		350
HEDG4	RPLQCWR	PGV	GVQGRRRGGT PGHLLPLRS SSSLERGMHM PTSPTFLEGN
HEDG4#36	RPLQCWR	PGV	GVQGRRRGGT PGHLLPLRS SSSLERGMHM PTSPTFLEGN
REDG4	RPLQCWR	PGV	GVQGRRRGGT PGHLLPLRS SSSLERGMHM PTSPTFLEGN
	351		
HEDG4	TVV~		
HEDG4#36	TVV~		
REDG4	TVV~		

10084507.022802

Figure 18A.

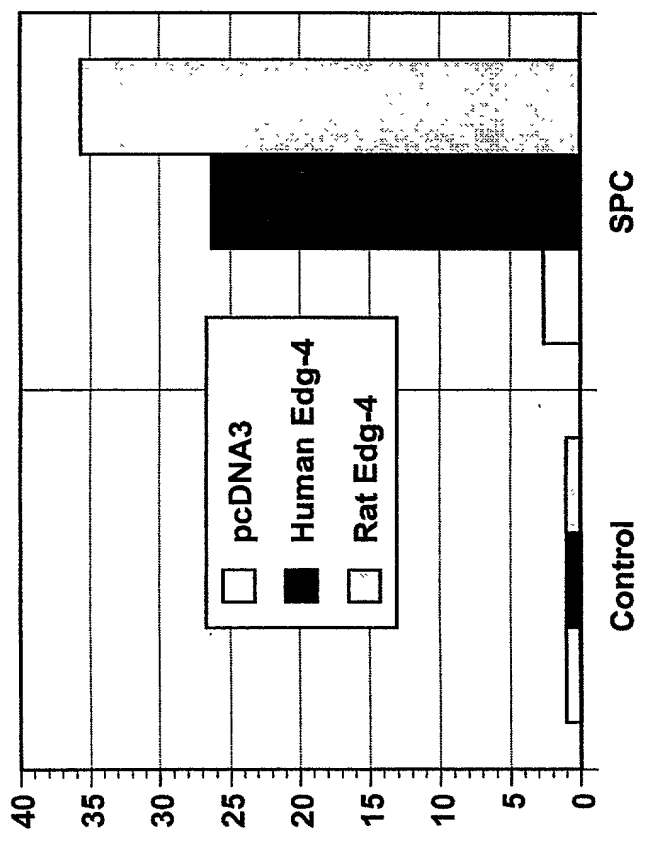


Figure 18B.

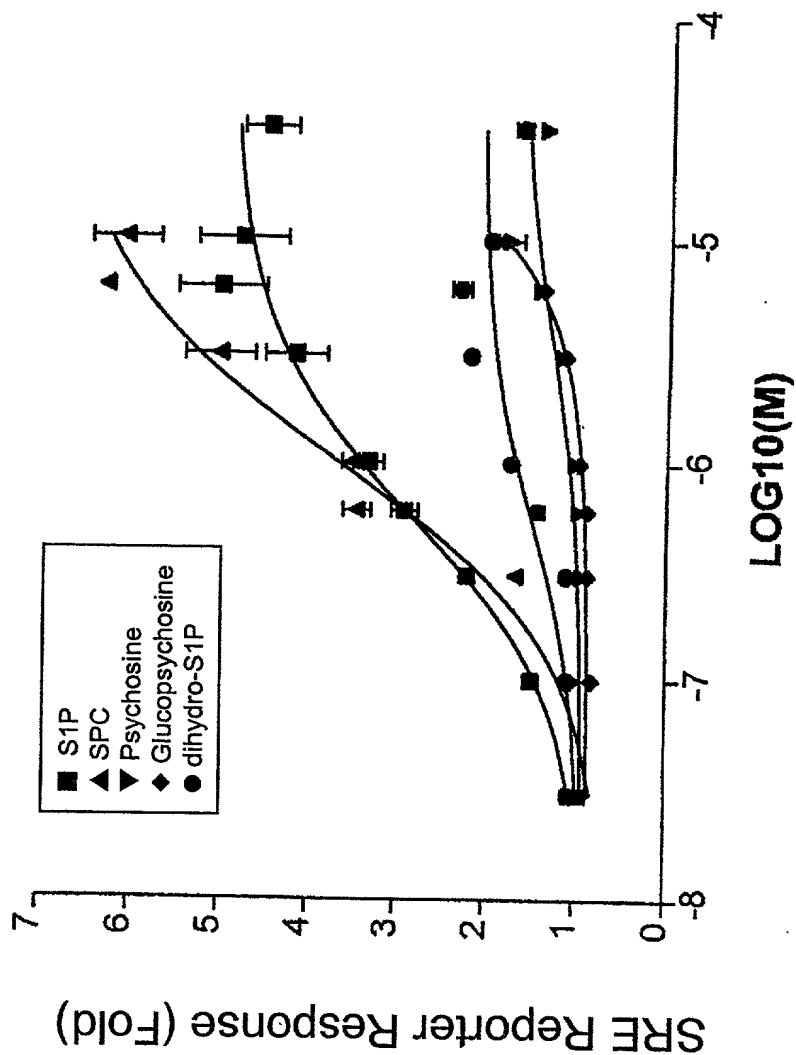


Figure 19.

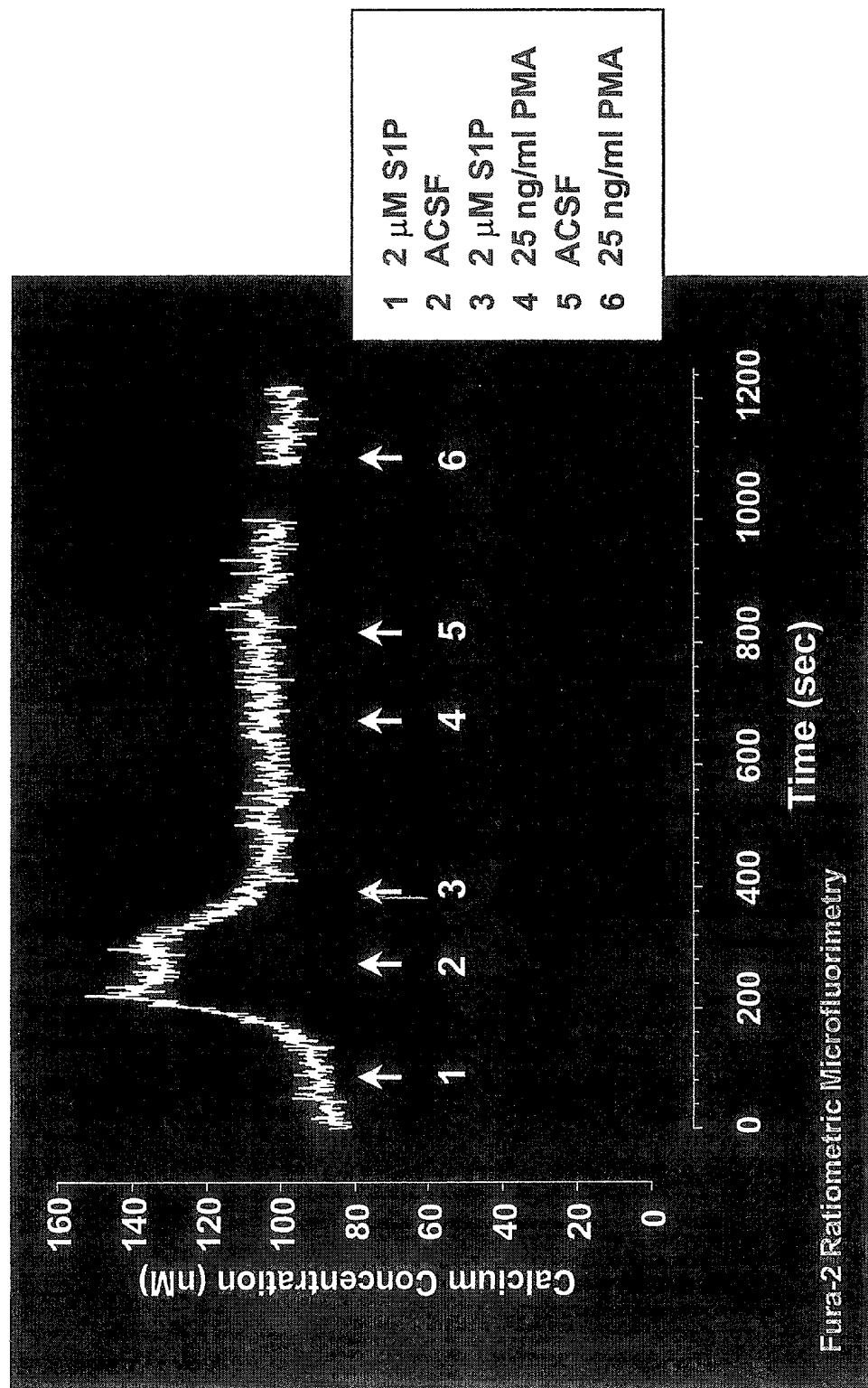


Figure 20.

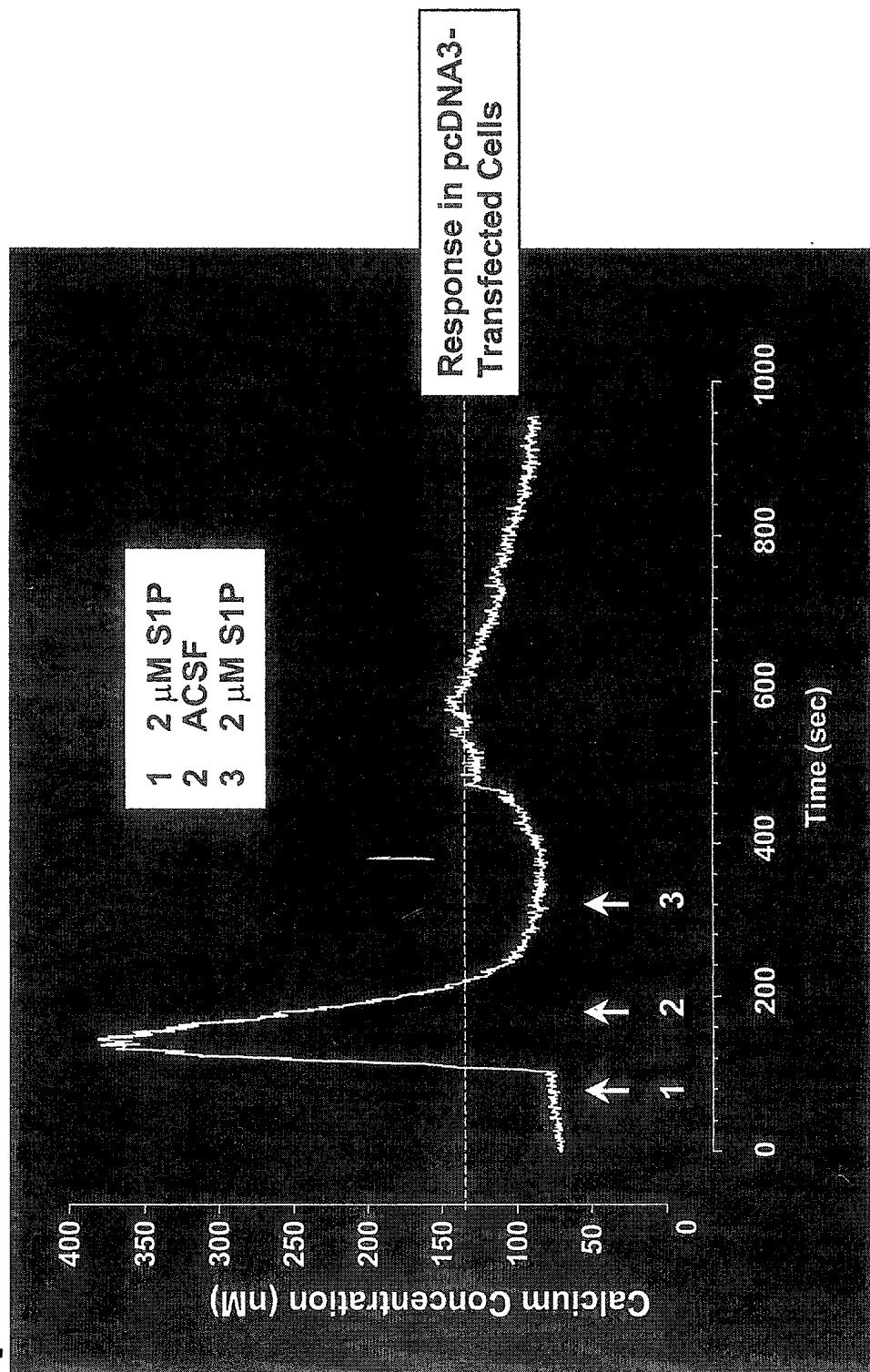


Figure 21. Human Edg-6 Amino Acid Sequence.

MVIMGQCYNETIGFFYNNSGKELSSHWRPKDVVVALGLTVSVLVLLTNLLVIAAIASN
1 -----+-----+-----+-----+-----+-----+ 60
RRFHQPIYYLLGNLAAADLFAGVAYLFLMFHTGPRTARLSLEGWFLRQGLLDTSLTASVA
61 -----+-----+-----+-----+-----+-----+ 120
TLLAIAVERHRSVMAVQLHSRLPRGRVVMLIVGVVVAALGLGLLPAHSWHCLCALDRCSR
121 -----+-----+-----+-----+-----+-----+ 180
MAPLLSRSYLAVWALSSLLVFLLMVAVYTRIFFYVRRRVQMAEHVSCHPRYRETTLSLV
181 -----+-----+-----+-----+-----+-----+ 240
KTVVILGAFVVCWTPGQVVLVLLDGLGCESC NVLAVEKYFLLLAEANSILVNAAVYSCRDA
241 -----+-----+-----+-----+-----+-----+ 300
EMRRTFRRLCCACL RQSTRESVHYTSSAQGGASTRIMLPENGHPLMDSTL*
301 -----+-----+-----+-----+-----+-----+ 352

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Figure 22. Human Edg-6 Sequence

1 ATGGTCATCATGGGCCAGTGCTACTACAACGAGACCATCGGCTTCTTCTATAACAACAGT 60
 -----+-----+-----+-----+-----+-----+
 TACCAGTAGTACCCGGTCACGATGATGTTGCTCTGGTAGCCGAAGAAGATATTGTTGTCA

 61 GGCAAAGAGCTCAGCTCCCACTGGCGGCCCAAGGATGTGGTCGTGGTGGCACTGGGGCTG 120
 -----+-----+-----+-----+-----+-----+
 CCGTTTCTCGAGTCGAGGGTGACCGCCGGGTTCTACACCAGCACCACCGTGACCCCGAC

 121 ACCGTCAGCGTGCTGGTGCTGCTGACCAATCTGCTGGTCATAGCAGCCATCGCCTCCAAC 180
 -----+-----+-----+-----+-----+-----+
 TGGCAGTCGCACGACCAGCAGACTGGTTAGACGACCAGTATCGTCGGTAGCGGAGGTTG

 181 CGCCGCTTCCACCAGCCCATCTACTACCTGCTCGGCAATCTGGCCGCGGCTGACCTCTTC 240
 -----+-----+-----+-----+-----+-----+
 GCGGCGAAGGTGGTCGGGTAGATGATGGACGAGCCGTTAGACCGGCGCCGACTGGAGAAG

 241 GCGGGCGTGGCCCTACCTCTTCCTCATGTTCCACACTGGTCCCCGCACAGCCCGACTTTCA 300
 -----+-----+-----+-----+-----+-----+
 CGCCCGCACCAGGATGGAGAAGGAGTACAAGGTGTGACCAGGGGCGTGTGCGGGCTGAAAGT

 301 CTTGAGGGCTGGTTCCCTGCGGCAGGGCTTGCTGGACACAAGCCTCACTGCGTCGGTGGCC 360
 -----+-----+-----+-----+-----+-----+
 GAACTCCCGACCAAGGACGCCGTCCCGAACGACCTGTGTTGCGAGTGACGCAGCCACCGG

 361 ACACTGCTGGCCATCGCCGTGGAGCGGCACCGCAGTGTGATGGCCGTGCAGCTGCACAGC 420
 -----+-----+-----+-----+-----+-----+
 TGTGACGACCGGTAGCGGCACCTCGCCGTGGCGTCACTACCGGCACGTGACGTGTGCG

 421 CGCCTGCCCCGTGGCCGCGTGGTCATGCTCATTGTGGGCGTGTGGGTGGCTGCCCTGGGC 480
 -----+-----+-----+-----+-----+-----+
 GCGGACGGGGCACCGGCGCACCAGTACGAGTAACACCCGCACACCCACCGACGGGACCCG

 481 CTGGGGCTGCTGCCTGCCACTCCTGGCACTGCCTCTGTGCCCTGGACCGCTGCTCACGC 540
 -----+-----+-----+-----+-----+-----+
 GACCCCGACGACGGACGGGTGAGGACCGTGACGGAGACACGGGACCTGGCGACGAGTGC

 541 ATGGCACCCCTGCTCAGCCGCTCCTATTTGGCCGTCTGGGCTCTGTGAGCCTGCTTGTC 600
 -----+-----+-----+-----+-----+-----+
 TACCGTGGGGACGAGTCGGCGAGGATAAACCGGCAGACCCGAGACAGCTCGGACGAACAG

 601 TTCCTGCTCATGGTGGCTGTGTACACCCGCATTTCTTCTACGTGCGGCGGCGAGTGCAG 660
 -----+-----+-----+-----+-----+-----+
 AAGGACGAGTACCACCGACACATGTGGGCGTAAAGAAGATGCACGCCGCCGCTCACGTC

 661 CGCATGGCAGAGCATGTCAGCTGCCACCCCGCTACCGAGAGACCACGCTCAGCCTGGTC 720
 -----+-----+-----+-----+-----+-----+
 GCGTACCGTCTCGTACAGTCGACCGTGGGGGCGATGGCTCTCTGCTGCGAGTCGGACCAG

 721 AAGACTGTTGTATCATCCTGGGGGCGTTCTGTTGCTGCTGGACACCAGGCCAGGTGGTA 780
 -----+-----+-----+-----+-----+-----+
 TTCTGACAACAGTAGTAGACCCCCGAAGCACCAGACGACCTGTGGTCCGGTCCACCAT

 781 CTGCTCCTGGATGGTTTAGGCTGTGAGTCCTGCAATGTCCTGGCTGTAGAAAAGTACTTC 840
 -----+-----+-----+-----+-----+-----+
 GACGAGGACCTACCAAATCCGACACTCAGGACGTTACAGGACCGACATCTTTTCATGAAG

202207254800T 10034507 022802

841 CTACTGcTGGCCGAGGCCAACTCACTGGTCAATGCTGCTGTGTACTCTTGCCGAGATGCT
 -----+-----+-----+-----+-----+-----+ 900
 GATGACgACCGGCTCCGGTTGAGTGACCAGTTACGACGACACATGAGAACGGCTCTACGA

 901 GAGATGCGCCGCACCTTCCGCCGCCTTCTCTGCTGCGCGTGCCTCCGCCAGTCCACCCGC
 -----+-----+-----+-----+-----+-----+ 960
 CTCTACGCGGCGTGGAAGGCGGCGGAAGAGACGACGCGCACGGAGGCGGTCAGGTGGGCG

 961 GAGTCTGTCCACTATACATCCTCTGCCCAGGGAGGTGCCAGCACTCGCATCATGCTTCCC
 -----+-----+-----+-----+-----+-----+ 1020
 CTCAGACAGGTGATATGTAGGAGACGGGTCCCTCCACGGTCGTGAGCGTAGTACGAAGGG

 1021 GAGAACGGCCACCCACTGATGGACTCCACCCTTTAG
 -----+-----+-----+-----+-----+ 1056
 CTCTTGCCGGTGGGTGACTACCTGAGGTGGGAAATC

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Figure 23.

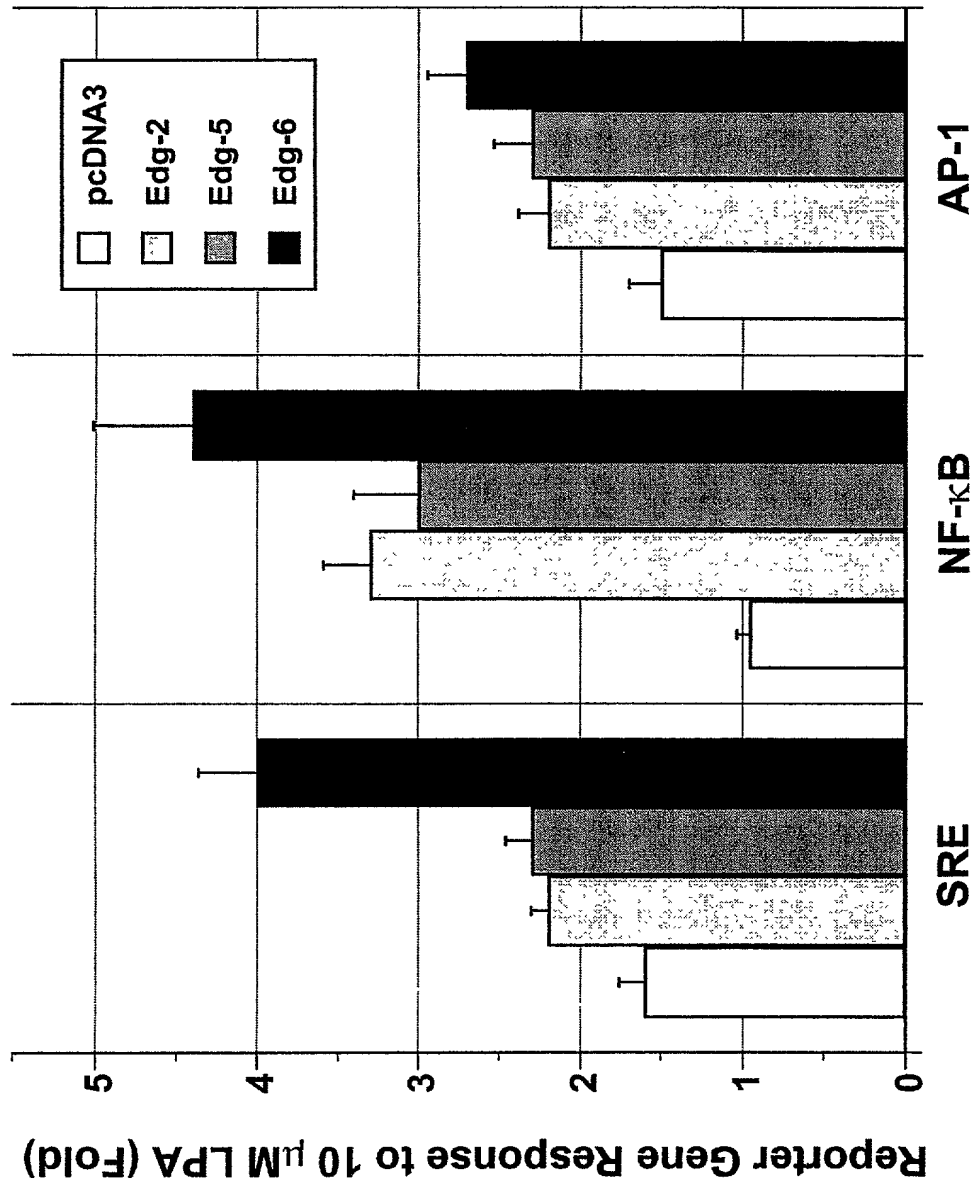


Figure 24.

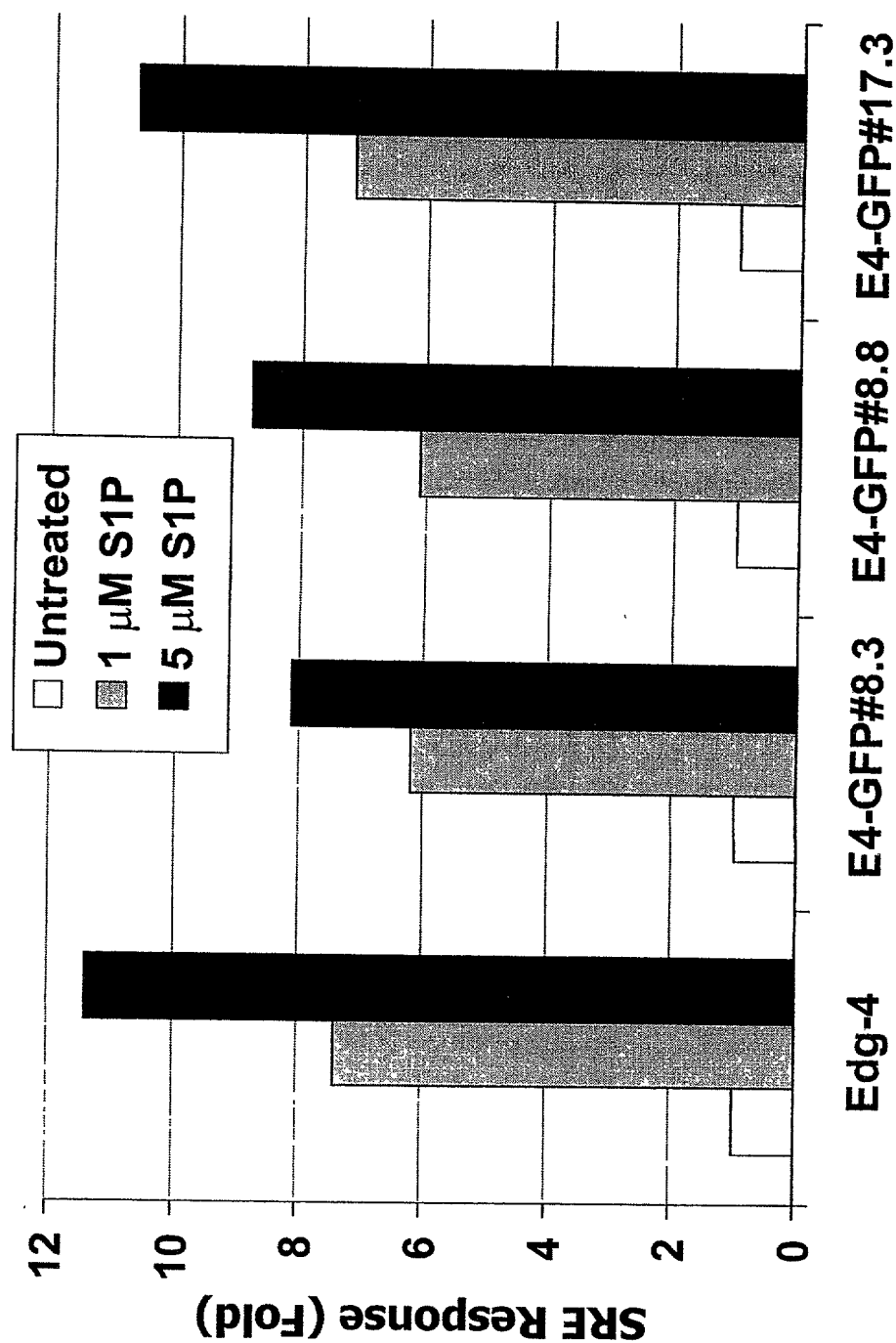
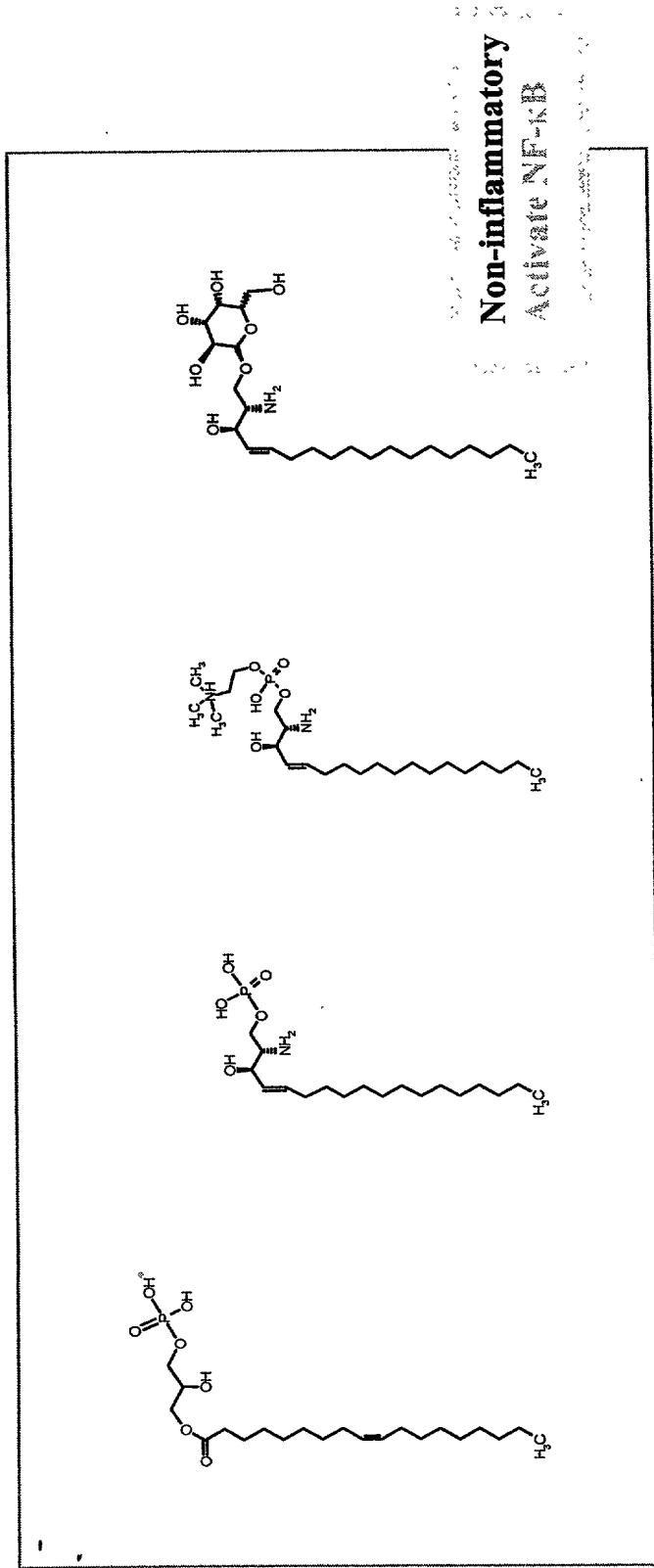


Figure 25.



Psychosine

SPC

S1P

LPA

15

Edg-1

د

Edg-7

Edg-1

THE

100

Edg-7

100

1. *Chlorophyll a* (Chl a) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum.

2002